AMENDMENTS

In the claims:

Please amend Claim 11 to read as follows.

1.(previously presented) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1.

2. (original) An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a) encodes the amino acid sequence shown in SEQ ID NO: 2; and

(b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

3.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.

4.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.

5. - 10. (cancelled)

11.(currently amended) An expression vector comprising [a] <u>the</u> nucleic acid sequence of Claim 4.

12.(previously presented) A cell comprising the expression vector of Claim 11.

RESPONSE

I. Status of the Claims

Claim 11 has been amended as suggested by the Examiner. Claims 1-4, 11 and 12 are pending .

II. Support for the Amended Claims

Amended Claim 11 finds support in original Claim 11 which found support in original Claim 4, throughout the specification as originally filed with particular support being found at least on page 13, lines 25-32.

As the amendments to Claim 11 are fully supported by the specification and claims as originally filed, they do not constitute new matter. Entry therefore is respectfully requested.

III. Rejection of Claims Under 35 U.S.C. § 112, Second Paragraph

Clam 11 stands rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Although Applicants in no way agree, in order to further progress this application towards allowance, Claim 11 has been amended exactly as the Examiner requested and thus this rejection has been avoided and Applicants' therefore request its withdrawal.

IV. Rejection of Claims Under 35 U.S.C. § 101

The rejection of claims 1-4, 11-12 under 35 U.S.C. § 101 is maintained because the claimed invention allegedly is not supported by either a specific and substantial asserted utility or a well-established utility. This rejection is respectfully traversed, based on the following arguments as well as those presented in earlier responses.

The rejection of claims 1-4 is maintained in this Final Action which again asserts that Applicants have failed to identify the function of the protein encoded by the sequences of the present invention and that therefore there can be no specific, substantial or credible utility.

The Final Action dismisses Applicants' continued assertions that the protein of the present invention is a human semaphorin protein and that semaphorin protein function is both <u>well known and implied</u> to those of skill in the art. The Action at page 3, line 5, cites Bork (Genome Research *10*:398-400, 2000) as supporting the proposition that prediction of protein function from homology information is somewhat unpredictable. However, a careful reading of Bork's publications and the other "relevant literature" does not in fact support the concept that function cannot be based on sequence and structural similarity, in contrast many of the examples actually support the use of such methodologies while identifying several areas in which caution should be exercised. These inaccuracies and potential pitfalls can be overcome by a more careful analysis by those of skill in the art. Automatic methods of sequence homology identification was only the staring point for consideration the sequences of the present invention underwent careful analysis by a series of individuals of skill in the art, many highly qualified (B.S. and Ph.D. level scientists).

These articles are merely examples of a small number of spurious publications that call into doubt the usefulness of bioinformatic predictions and that the PTO has repeatedly attempted to use as a basis to deny the utility of nucleic acid sequences. However, without going into the merits (or lack thereof) of all of the cited articles, Appellants point out that the lack of 100% unanimous agreement on the usefulness of bioinformatic prediction programs is completely irrelevant to the question of whether the claimed nucleic acid sequence has a substantial and specific utility. Appellants respectfully point out that the legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be **<u>believable</u>**. Appellants submit that the overwhelming majority of those of skill in the relevant art would **<u>believe</u>** bioinformatic prediction to be a powerful and useful tool, as evidenced by hundreds if not thousands of journal articles.

Rather, the question of utility is a straightforward one. As set forth by the Federal Circuit, "(t)he threshold of utility is not high: An invention is 'useful' under section 101 if it is capable of providing some identifiable benefit." *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700 (Fed. Cir. 1999) (citing *Brenner v. Manson*, 383 U.S. 519, 534 (1966)). Additionally, the Federal Circuit has stated that "(t)o violate § 101 the claimed device must be <u>totally incapable</u> of achieving a useful result." *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992), emphasis added. *Cross v. Iizuka* (224 USPQ 739 (Fed. Cir. 1985); "*Cross*") states "<u>any</u> utility of the claimed compounds is sufficient to satisfy 35 U.S.C. § 101". *Cross* at 748, emphasis added.

Indeed, the Federal Circuit recently emphatically confirmed that "anything under the sun that is made by man" is patentable *(State Street Bank & Trust Co. v. Signature Financial Group Inc.*, 47 USPQ2d 1596, 1600 (Fed. Cir. 1998), citing the U.S. Supreme Court's decision in *Diamond vs. Chakrabarty*, 206 USPQ 193 (S.Ct. 1980)).

The legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be credible or believable. According to the Examination Guidelines for the Utility Requirement, if the applicant has asserted that the claimed invention is useful for any particular purpose (i.e., it has a "specific and substantial utility") and the assertion would be considered credible by a person of ordinary skill in the art, the Examiner should not impose a rejection based on lack of utility (66 Federal Register 1098, January 5, 2001).

As evidence of the credibility of Applicants assertion that the present invention is a variant of human semaphorin sem 2, In Applicants' response to the First Office Action (Paper No. 13) Applicants' submitted an amino acid sequence comparison between SEQ ID NO: 3 and BAA98132 (as Exhibit E), which was annotated by third party scientists, wholly unaffiliated with Applicants, as encoding semaphorin sem2 [Homo sapiens] (BAA98132: as Exhibit F). In this submission was included evidence that SEQ ID NO: 1 (see previously submitted Exhibit G comparing SEQ ID NOS: 3 and 1) identifies a longer isoform of the present invention, which is clearly encoded by the same genetic locus. Clearly those of skill in the art would recognize the sequences of the present invention as encoding a human semaphorin. As evidenced by the review article entitled "Molecular Mechanisms of Axonal Guidance" from the prestigious journal Science (298:1959-1964, 2002 and erratum; previously submitted as Exhibit H in Paper No. 13), semaphorins are well known to those of skill in the art as soluble and membrane-bound proteins that act as chemorepulsive factors in neuronal development, thereby playing a crucial role in axon guidance. Semaphorins, such as the one described in the present invention, provide guidance for neuronal growth. In the second paragraph of Section 5.1 or the specification as filed, it is stated that "Because of their role in neural development, semaphorins have been subject to considerable scientific scrutiny. For example, U.S. Patents Nos. 5,981,222 and 5,935,865, both of which are herein incorporated by reference, describe other semaphorins as well as applications, utilities". Therefore, clearly, there can be no question that Applicants' asserted identity and utility for the described sequences a semaphorin is "credible." In addition, those of skill in the art in the biomedical and pharmaceutical industry would readily recognize the utility for semaphorins and

their application to medical conditions requiring nerve regeneration. For example, the regeneration and repair of nerve tissue following the surgical attachment of severed limbs or the resection of diseased tissue, as well as nerve repair following a stroke.

Further support of Applicants' position that the function of the protein encoded by the sequences of the present invention is that of semaphorin sem 2 is further provided by the nucleotide sequence encoding the previously presented protein (BAA98132) shares 99.957 % percent homology over the entire nucleic acid sequence of SEQ ID NO:3 (nucleic acid alignment presented as **New Exhibit AA**; GenBank accession number AB029496).

Applicants have thus supplied evidence supporting their assertion that those of skill in the art would recognize that the sequences of the present invention encode variants of human semaphorin. Applicant's assertion also supports a "well-established" utility in that persons of ordinary skill in the art would immediately appreciate. In contrast, the Examiner has provided no evidence of record indicating that those of skill in the art would not recognize the sequences of the present invention encode semaphorin. As such, the scientific evidence clearly establishes that Applicants have described an invention whose utility is in full compliance with the provisions of 35 U.S.C. § 101, and therefore Applicants respectfully request withdrawal of the rejection.

The Final Action states that there is no disclosure in the specification suggesting that the sequences of the present invention as encoding the biological activity of human semaphorins (page 3 lines 9-10). However, the application clearly identifies similarities between the sequences of the present invention (SEQ ID NOS: 1-5) and semaphorin proteins (at least on page 2, lines 14-15; page 4, lines 10-11 and page 17, line 10) and their tissue expression distribution (page 4, lines 10-15) and describes the activity of semaphorins (page 4, lines 10-15) and <u>well-established</u> utility "Because of their role in neural development, semaphorins have been subject to considerable scientific scrutiny. For example, U.S. Patents Nos. 5,981,222 and 5,935,865, both of which are herein incorporated by reference, describe other semaphorins as well as applications, utilities, and uses ..." (page 17, lines 14-18). Clearly Applicants were aware at the time of filing of the semaphorin like nature of the protein encoded by sequences of the present invention.

Furthermore the Examiner's position that mere homology of SEQ ID No:1 to a known DNA molecule with a known function does not endow SEQ ID NO:1 with the function is contrary to Example 10 of the PTO's Revised Interim Utility Guidelines Training Materials (pages 53-55), which

establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and under 35 U.S.C. § 112, first paragraph as allegedly unusable by the skilled artisan due to the alleged lack of patentable utility, is not proper when there is no reason to doubt the asserted utility of a full length sequence (such as the presently claimed sequence) that has a similarity score of 95% to a protein having a known function. In the Analysis portion of Example 10 it states that "Based on applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO:2 encodes a DNA ligase. Further DNA ligases have a well-established use in the molecular biology art based on this class of proteins ability to ligate DNA. ......Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed...... Thus the conclusion reached from this analysis is that a 35 U.S.C. § 101 and a 35 U.S.C. § 112 first paragraph, utility rejection should not be made."

The present case is similar to that presented in Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55). In the present case it is clear that the sequences of the present invention encode a semaphorin. Semaphorins have a well-established function. Thus a 35 U.S.C. § 101 and a 35 U.S.C. § 112 first paragraph, utility rejection should not have been made and should therefore, be withdrawn.

As set forth in *In re Langer* (183 USPQ 288 (CCPA 1974); "*Langer*"):

> As a matter of Patent Office practice, a specification which contains a disclosure of utility which corresponds in scope to the subject matter sought to be patented must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is a reason for one skilled in the art to question the objective truth of the statement of utility or its scope.

Langer at 297, emphasis in original. As set forth in the MPEP, "Office personnel must provide evidence sufficient to show that the statement of asserted utility would be considered 'false' by a person of ordinary skill in the art" (MPEP, Eighth Edition at 2100-40, emphasis added). Thus, absent such evidence from the Examiner concerning the role of the presently claimed sequence encodes a protein kinase, the present claims clearly meet the requirements of 35 U.S.C. § 101.

The Action also disregards Applicant's asserted utility of the presently claimed polynucleotides on DNA chips (Action at page 3, Section 4.(ii)). Further, the Action seems to be requiring Applicants to identify the biological role of the nucleic acid or function of the protein encoded by the presently claimed polynucleotides before the present sequences can be used in gene chip applications that meet

the requirements of § 101. Applicants respectfully point out that knowledge of the exact function or role of the presently claimed sequence <u>is not required</u> to track expression patterns using a DNA chip. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. Particularly as Applicants have identified the protein encoded as a semaphorin, identified the specific tissues in which this gene is expressed (page 4, lines 10-15) and identified a specific polymorphism in SEQ ID NO:1 (page 17, lines 8-18). The claimed sequence provides a <u>specific</u> marker of the human genome (see evidence below), and that such <u>specific</u> markers are targets for discovering drugs that are associated with human disease. Thus, those skilled in the art would instantly recognize that the present nucleotide sequence would be an ideal, novel candidate for assessing gene expression using, for example, DNA chips, as the specification details. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, as well as more recently issued U.S. Patent Nos. 5,837,832, 6,156,501 and 6,261,776. Accordingly, the present sequence has a <u>specific</u> utility in such DNA chip applications. Clearly, compositions that <u>enhance</u> the utility of such DNA chips, such as the presently claimed nucleotide sequence, must also be useful.

Additionally, since only a small percentage of the genome (2-4%) actually encodes exons, which in-turn encode amino acid sequences. Thus, not all human genomic DNA sequences are useful in such gene chip applications. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101. It has been clearly established that a statement of utility in a specification must be accepted absent reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971).

Evidence of the "real world" <u>substantial</u> utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company, Rosetta Inpharmatics, was viewed to have such "real world" value that it was acquired by large pharmaceutical company, Merck & Co., for substantial

sums of money (net equity value of the transaction was $620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, 2001, Science *291*:1304). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, 2001, Science *291*:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years). The use of the claimed polypeptide in an array for screening purposes Applicants respectfully point out that nucleic acid sequences have the greatest specific utility in gene chip applications once the role of the sequence has been identified, as have tissues of interest, as in the present case. Once the role of the particular nucleic acid is known, the level of gene expression has and even greater significance. By identifying the physiological activity role of the claimed sequence, the claimed sequence has a far greater utility in gene chip applications that just any random piece of DNA.

As a still further example of utility is the use of the present sequences in such diagnostic assays (at least at page 9, line 7; page 18 line 11; page 25, line 32) as those associated with identification of paternity and forensic analysis, among others. The sequences of the present invention have particular utility as the application as filed identified a polymorphism in SEQ ID NO:1 (page 17, lines 8-18). This is also not a case of a potential utility. Appellants respectfully submit that even in the worst case scenario, the described polymorphisms are each useful to distinguish 50% of the population (in other words, the marker being present in half of the population) and that the ability of a polymorphic marker to distinguish at least 50% of the population is an inherent feature of any polymorphic marker, and this feature is well understood by those of skill in the art. Appellants note that as a matter of law, it is well settled that a patent need not disclose what is well known in the art. *In re Wands*, 8 USPQ 2d 1400 (Fed. Cir. 1988). Appellants support for Appellants' assertion of utility is provided by the fact that the skilled artisan would readily recognize and easily believe that the presently described polymorphic markers could be useful in forensic analysis. The fact that forensic biologists use polymorphic markers

such as those described by Appellants <u>every day</u> provides more that ample support for the assertion that forensic biologists would also be able to use the specific polymorphic markers described by Appellants in the same fashion. Therefore, again it is clear that the sequences of the present invention have utility.

Applicants respectfully submit that **<u>specific</u>** utility, which is the proper standard for utility under 35 U.S.C. § 101, is distinct from the requirement for a **<u>unique</u>** utility, which is clearly an <u>improper</u> standard. As clearly stated by the Federal Circuit in *Carl Zeiss Stiftung v. Renishaw PLC*, 20 USPQ2d 1101 (Fed. Cir. 1991; "*Carl Zeiss*"):

> An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: "[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding a lack of utility." *Envirotech Corp. v. Al George, Inc.*, 221 USPQ 473, 480 (Fed. Cir. 1984)

Therefore, just because other nucleic acid sequences find utility in gene chip applications does not mean that the use of Applicants' sequence in gene chip applications is not a <u>specific</u> utility. Furthermore, the requirement for a unique utility is clearly not the standard adopted by the Patent and Trademark Office. If every invention were required to have a unique utility, the Patent and Trademark Office would no longer be issuing patents on batteries, automobile tires, golf balls, golf clubs, and treatments for a variety of human diseases, such as cancer and bacterial or viral infections, just to name a few particular examples, because examples of each of these have already been described and patented. All batteries have the exact same utility - specifically, to provide power. All automobile tires have the exact same utility - specifically, for use on automobiles. All golf balls and golf clubs have the exact same utility - specifically, use in the game of golf. All cancer treatments have the exact same utility - specifically, to treat cancer. All anti-infectious agents have the exact same broader utility - specifically, to treat infections. However, only the briefest perusal of virtually any issue of the Official Gazette provides numerous examples of patents being granted on each of the above compositions <u>every week</u>. Furthermore, if a composition needed to be unique to be patented, the entire class and subclass system would be an effort in futility, as the class and subclass system serves solely to group such common inventions, which would not be required if each invention needed to have a <u>unique</u> utility. Thus, the present sequence clearly meets the requirements of 35 U.S.C. § 101.

The Action further discounts the utility of the claimed sequence for exon mapping as there is "no knowledge of what the function of the actual sequence, regardless of the basis of homology, then there is no asserted utility"(Final Action Page 4, line 4-6). Applicants respectfully submit that the function of the sequence as a semaphorin and several utilities were asserted in the application as filed (addressed above).

Although Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), as a further example of the utility of the presently claimed polynucleotides, as described in the specification at least at page 12 lines 4-10, the present nucleotide sequence has a specific utility in determining the genomic structure of the corresponding human chromosome, for example mapping the protein encoding regions. As evidence supporting Applicants assertions of the specific utility of the sequences of the present invention in localizing the specific region of the human chromosome and identification of functionally active intron/exon splice junctions is the information provided as Exhibit BB. This is the result of overlaying the sequence of SEQ ID NO:1 of the present invention and the identified human genomic sequence. By doing this, one is able to identify the portions of the genome that encode the present invention. As these regions of the genome are non-contiguous, this is indicative of individual exons. The results of such an analysis indicate that the sequence of the present invention is the result of a 16 exon gene contained within the BAC clone AC006208.3. Clearly as the gene of the present invention is encoded by 16 non-contiguous exons on chromosome 3, one would not have been able to deduce the sequence that encodes the molecules of the present invention without knowing the sequence. Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of human chromosome 3 that contains the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences. In fact, it is this specificity that makes this particular sequence so useful.

Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the

human genome, such as the present nucleic acid sequence. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Equally significant is that the claimed polynucleotide sequences define how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The presently claimed sequence clearly identified the intron/exon boundaries, as described above. The specification details that "sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (*e.g.*, splice acceptor and/or donor sites), *etc.*, that can be used in diagnostics and pharmacogenomics" (specification at page 8, lines 14-20). Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Applicants again draw attention to the distinction between the requirements of a specific utility with a unique utility. The fact that a small number of other nucleotide sequences could be used to map the protein coding regions in this specific region of chromosome 3 does not mean that the use of Applicants' sequence to map the protein coding regions of chromosome 3 is not a specific utility (*Carl Zeiss Stiftung v. Renishaw PLC, supra*).

Finally, while Applicants are well aware of the new Utility Guidelines set forth by the USPTO, it has been long established that the current rules regarding the examination of patent applications is and always has been the patent laws as set forth in 35 U.S.C. and the patent rules as set forth in 37 C.F.R., not the Manual of Patent Examination Procedure or particular guidelines for patent examination set forth by the USPTO. Furthermore, it is the job of the judiciary, not the USPTO, to interpret these laws and rules. Applicants point out that guidelines that are not consistent with the patent laws, or the interpretation of these laws by the judicial branch, are not the final word in determining whether or not claims comply with any particular section of the patent laws. Applicants are unaware of any significant recent changes in either 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit that is in keeping with the new Utility Guidelines set forth by the USPTO. This is underscored by numerous patents that have been issued over the years that claim nucleic acid fragments that do not comply with the new Utility Guidelines. As examples of such issued U.S. Patents, the Examiner is invited to review U.S. Patent Nos. 5,817,479, 5,654,173, and 5,552,281 (each of which claim short polynucleotides), none of which contain examples of the "real-world" utilities that

seem to be required in the Action. As issued U.S. Patents are presumed to meet all of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph (see Section III, below), Applicants submit that the presently claimed polynucleotides must also meet the requirements of 35 U.S.C. § 101. While Applicants understand that each patent application is examined on the basis of its individual merits, Applicants are unaware of any changes to 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit, since the issuance of these patents that render the subject matter claimed in these patents, which is similar to the subject matter in question in the present application, as suddenly non-statutory or failing to meet the requirements of 35 U.S.C. § 101. The requirement of Applicants to meet a different standard of utility in the present case would be arbitrary and capricious, and cannot stand.

In summary, the present situation is similar to Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55), which establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and under 35 U.S.C. § 112, first paragraph as allegedly unusable by the skilled artisan due to the alleged lack of patentable utility, is not proper when the full length sequence of the invention encodes a protein that has a well known function. Furthermore this response has described a series of additional substantial, specific, credible and well-established utilities for the present invention in addition to those described in Applicants' many previous responses. Therefore, Applicants submit that as the presently claimed sequence molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of the claims under 35 U.S.C. § 101 has been overcome. Thus, Applicants respectfully request that the rejection be withdrawn.

V. Rejection of Claims Under 35 U.S.C. § 112, First Paragraph

Claims 1-4, 11-12 are also rejected under 35 U.S.C. § 112 first paragraph. Specifically, since the claimed invention is not supported by either specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Applicants submit that all claims have been shown to have "a specific, substantial, and credible utility", as detailed above. Applicants therefore request that the rejection of all claims under 35 U.S.C. § 112, first paragraph, be withdrawn.

VI. Rejection of Claims Under 35 U.S.C. § 101 & 35 U.S.C. § 112

Claims 11-12 are rejected under the above 35 U.S.C. § 101 and 35 U.S.C. § 112, first paragraph, allegedly based on the same reasoning as above. As claims 11 and 12 are dependent upon Claim 4 and Claim 4 has now been shown to have a patentable utility under 35 U.S.C. Sections 101 and 112, this rejection has been avoided and Applicants, therefore, request withdrawal of the rejection.

VII. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Chism have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

September 22, 2003
Date

L K Ishimoto by Peter G Seferian Reg No. 60162

Lance K. Ishimoto Reg. No. 41,866

LEXICON GENETICS INCORPORATED
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Customer # 24231

Exhibit AA

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 FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAWTaiDv: 2349 nt
 >LEX151 SEQ ID NO:3
 vs  /tmp/fastaDAAXTaiDv library
searching /tmp/fastaDAAXTaiDv library

   4700 residues in     1 sequences

FASTA (3.34 January 2000) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
 join: 74, opt: 59, gap-pen: -16/ -4, width:  16
 Scan time:  0.100
The best scores are:                                              opt
gi|8978201|dbj|AB029496.1| Homo sapiens mRNA f (4700) [f] 11742
gi|8978201|dbj|AB029496.1| Homo sapiens mRNA f (4700) [r]    78

>>gi|8978201|dbj|AB029496.1| Homo sapiens mRNA for semap  (4700 nt)
 initn: 11742 init1: 11742 opt: 11742
 99.957% identity in 2349 nt overlap (1-2349:1-2349)

               10        20        30        40        50        60
LEX151 ATGGCCCCCTCGGCCTGGGCCATTTGCTGGCTGCTAGGGGGCCTCCTGCTCCATGGGGGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 ATGGCCCCCTCGGCCTGGGCCATTTGCTGGCTGCTAGGGGGCCTCCTGCTCCATGGGGGT
               10        20        30        40        50        60

               70        80        90       100       110       120
LEX151 AGCTCTGGCCCCAGCCCCGGCCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 AGCTCTGGCCCCAGCCCCGGCCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTC
               70        80        90       100       110       120

              130       140       150       160       170       180
LEX151 CTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCC
              130       140       150       160       170       180

              190       200       210       220       230       240
LEX151 ATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 ATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCT
              190       200       210       220       230       240

              250       260       270       280       290       300
LEX151 CTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAGCCAGGA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAGCCAGGA
              250       260       270       280       290       300

              310       320       330       340       350       360
LEX151 CAGAGGGAGGAGTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CAGAGGGAGGAGTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTG
              310       320       330       340       350       360

              370       380       390       400       410       420
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LEX151 CGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTCCAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTCCAG
                370       380       390       400       410       420

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LEX151 CCCACCTGTGCCCTCATCACAGTTGGCCACCGTGGGGAGCATGTGCTCCACCTGGAGCCT
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LEX151 GGCAGTGTGGAAAGTGGCCGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGC
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               1210      1220      1230      1240      1250      1260
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            Miyajima,N. and Saito,T.
  TITLE     Human semaphorin
  JOURNAL   Published Only in DataBase (2000)
REFERENCE   2  (bases 1 to 4700)
  AUTHORS   Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
            Miyajima,N. and Saito,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1999) Toshiyuki Saito, National Institute of
            Radiological Sciences, Genome Research Group; Inage-ku Anagawa
            4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
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4561 gtgagaaaag ctgaatttac aaggaaaggg atgaagttaa tatttgcatc acataattat
4621 atcattactg tgtatctgtg tattgtacta aatggactga tgctgcgcac atgagctgaa
4681 aatgaagagc cctcccatcc
//
```

```
 FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAAL1aqDv: 2628 nt
 >LEX151 SEQ ID NO:1
 vs  /tmp/fastaHAAM1aqDv library
searching /tmp/fastaHAAM1aqDv library

   4700 residues in     1 sequences

FASTA (3.34 January 2000) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
 join: 77, opt: 62, gap-pen: -16/ -4, width:  16
 Scan time:  0.117
The best scores are:                                          opt
gi|8978201|dbj|AB029496.1| Homo sapiens mRNA f (4700) [f] 11742
gi|8978201|dbj|AB029496.1| Homo sapiens mRNA f (4700) [r]    95

>>gi|8978201|dbj|AB029496.1| Homo sapiens mRNA for semap  (4700 nt)
 initn: 11742 init1: 11742 opt: 11742
 99.957% identity in 2349 nt overlap (280-2628:1-2349)

     250       260       270       280       290       300
LEX151 AGGCGGCAGCGGTGCCCTCAGTTCCCCAGCATGGCCCCCTCGGCCTGGGCCATTTGCTGG
                                     ::::::::::::::::::::::::::::::
gi|897                               ATGGCCCCCTCGGCCTGGGCCATTTGCTGG
                                             10        20        30

     310       320       330       340       350       360
LEX151 CTGCTAGGGGGCCTCCTGCTCCATGGGGGTAGCTCTGGCCCCAGCCCCGGCCCCAGTGTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGCTAGGGGGCCTCCTGCTCCATGGGGGTAGCTCTGGCCCCAGCCCCGGCCCCAGTGTG
                     40        50        60        70        80        90

     370       380       390       400       410       420
LEX151 CCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTG
                    100       110       120       130       140       150

     430       440       450       460       470       480
LEX151 GGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGACCGCCTC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGACCGCCTC
                    160       170       180       190       200       210

     490       500       510       520       530       540
LEX151 TTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 TTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCC
                    220       230       240       250       260       270

     550       560       570       580       590       600
LEX151 CGGGAGGTCCTGTGGCCACCGCAGCCAGGACAGAGGGAGGAGTGTGTTCGAAAGGGAAGA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CGGGAGGTCCTGTGGCCACCGCAGCCAGGACAGAGGGAGGAGTGTGTTCGAAAGGGAAGA
                    280       290       300       310       320       330

     610       620       630       640       650       660
```

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LEX151  GATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCACAACCGGACCCAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCACAACCGGACCCAC
                    340       350       360       370       380       390

     670       680       690       700       710       720
LEX151  CTGCTAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CTGCTAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCAC
                    400       410       420       430       440       450

     730       740       750       760       770       780
LEX151  CGTGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGAAAGTGGCCGGGGGCGGTGC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CGTGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGAAAGTGGCCGGGGGCGGTGC
                    460       470       480       490       500       510

     790       800       810       820       830       840
LEX151  CCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGT
                    520       530       540       550       560       570

     850       860       870       880       890       900
LEX151  CTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCA
                    580       590       600       610       620       630

     910       920       930       940       950       960
LEX151  GCTCTGCGTTCCGACTCTGACCAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GCTCTGCGTTCCGACTCTGACCAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCC
                    640       650       660       670       680       690

     970       980       990      1000      1010      1020
LEX151  CGGATCCCTGAGAACTCTGACCAGGACAATGACAAGGTGTACTTCTTCTTCTCGGAGACG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CGGATCCCTGAGAACTCTGACCAGGACAATGACAAGGTGTACTTCTTCTTCTCGGAGACG
                    700       710       720       730       740       750

    1030      1040      1050      1060      1070      1080
LEX151  GTCCCCTCGCCCGATGGTGGCTCGAACCATGTCACTGTCAGCCGCGTGGGCCGCGTCTGC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GTCCCCTCGCCCGATGGTGGCTCGAACCATGTCACTGTCAGCCGCGTGGGCCGCGTCTGC
                    760       770       780       790       800       810

    1090      1100      1110      1120      1130      1140
LEX151  GTGAATGATGCTGGGGGCCAGCGGGTGCTGGTGAACAAATGGAGCACTTTCCTCAAGGCC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GTGAATGATGCTGGGGGCCAGCGGGTGCTGGTGAACAAATGGAGCACTTTCCTCAAGGCC
                    820       830       840       850       860       870

    1150      1160      1170      1180      1190      1200
LEX151  AGGCTGGTCTGCTCGGTGCCCGGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  AGGCTGGTCTGCTCGGTGCCCGGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAG
                    880       890       900       910       920       930

    1210      1220      1230      1240      1250      1260
```

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LEX151  GATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGC
                  940       950       960       970       980       990

          1270      1280      1290      1300      1310      1320
LEX151  ACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGTGTGTACCACATGGCAGACATCTGG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  ACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGTGTGTACCACATGGCAGACATCTGG
                 1000      1010      1020      1030      1040      1050

          1330      1340      1350      1360      1370      1380
LEX151  GAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGCCCTAT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGCCCTAT
                 1060      1070      1080      1090      1100      1110

          1390      1400      1410      1420      1430      1440
LEX151  GGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGCCCCAGCAAGATGACCGCACAGCCA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGCCCCAGCAAGATGACCGCACAGCCA
                 1120      1130      1140      1150      1160      1170

          1450      1460      1470      1480      1490      1500
LEX151  GGACGGCCTTTTGGCAGCACCAAGGACTACCCAGATGAGGTGCTGCAGTTTGCCCGAGCC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GGACGGCCTTTTGGCAGCACCAAGGACTACCCAGATGAGGTGCTGCAGTTTGCCCGAGCC
                 1180      1190      1200      1210      1220      1230

          1510      1520      1530      1540      1550      1560
LEX151  CACCCCCTCATGTTCTGGCCTGTGCGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CACCCCCTCATGTTCTGGCCTGTGCGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACC
                 1240      1250      1260      1270      1280      1290

          1570      1580      1590      1600      1610      1620
LEX151  CACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGTGGAGGCAGAGGATGGGACC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGTGGAGGCAGAGGATGGGACC
                 1300      1310      1320      1330      1340      1350

          1630      1640      1650      1660      1670      1680
LEX151  TACGATGTCATTTTCCTGGGGACTGACTCAGGGTCTGTGCTCAAAGTCATCGCTCTCCAG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  TACGATGTCATTTTCCTGGGGACTGACTCAGGGTCTGTGCTCAAAGTCATCGCTCTCCAG
                 1360      1370      1380      1390      1400      1410

          1690      1700      1710      1720      1730      1740
LEX151  GCAGGGGGCTCAGCTGAACCTGAGGAAGTGGTTCTGGAGGAGCTCCAGGTGTTTAAGGTG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  GCAGGGGGCTCAGCTGAACCTGAGGAAGTGGTTCTGGAGGAGCTCCAGGTGTTTAAGGTG
                 1420      1430      1440      1450      1460      1470

          1750      1760      1770      1780      1790      1800
LEX151  CCAACACCTATCACCGAAATGGAGATCTCTGTCAAAAGGCAAATGCTATACGTGGGCTCT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897  CCAACACCTATCACCGAAATGGAGATCTCTGTCAAAAGGCAAATGCTATACGTGGGCTCT
                 1480      1490      1500      1510      1520      1530

          1810      1820      1830      1840      1850      1860
```

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LEX151 CGGCTGGGTGTGGCCCAGCTGCGGCTGCACCAATGTGAGACTTACGGCACTGCCTGTGCA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CGGCTGGGTGTGGCCCAGCTGCGGCTGCACCAATGTGAGACTTACGGCACTGCCTGTGCA
             1540      1550      1560      1570      1580      1590

     1870      1880      1890      1900      1910      1920
LEX151 GAGTGCTGCCTGGCCCGGGACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCCACTAC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GAGTGCTGCCTGGCCCGGGACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCCACTAC
             1600      1610      1620      1630      1640      1650

     1930      1940      1950      1960      1970      1980
LEX151 CGCCCCAGCCTTGGCAAGCGCCGGTTCCGCCGGCAGGACATCCGGCACGGCAACCCTGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CGCCCCAGCCTTGGCAAGCGCCGGTTCCGCCGGCAGGACATCCGGCACGGCAACCCTGCC
             1660      1670      1680      1690      1700      1710

     1990      2000      2010      2020      2030      2040
LEX151 CTGCAGTGCCTGGGCCAGAGCCAGGAAGAAGAGGCAGTGGGACTTGTGGCAGCCACCATG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGCAGTGCCTGGGCCAGAGCCAGGAAGAAGAGGCAGTGGGACTTGTGGCAGCCACCATG
             1720      1730      1740      1750      1760      1770

     2050      2060      2070      2080      2090      2100
LEX151 GTCTACGGCACGGAGCACAATAGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCARGCT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::.:::
gi|897 GTCTACGGCACGGAGCACAATAGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCAGGCT
             1780      1790      1800      1810      1820      1830

     2110      2120      2130      2140      2150      2160
LEX151 GCTGTGCGCTGGCTCTTGCAGAGGCCAGGGGATGAGGGGCCTGACCAGGTGAAGACGGAC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GCTGTGCGCTGGCTCTTGCAGAGGCCAGGGGATGAGGGGCCTGACCAGGTGAAGACGGAC
             1840      1850      1860      1870      1880      1890

     2170      2180      2190      2200      2210      2220
LEX151 GAGCGAGTCTTGCACACGGAGCGGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GAGCGAGTCTTGCACACGGAGCGGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCG
             1900      1910      1920      1930      1940      1950

     2230      2240      2250      2260      2270      2280
LEX151 GGCACCTACACCTGCACCACTCTGGAGCATGGCTTCTCCCAGACTGTGGTCCGCCTGGCT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GGCACCTACACCTGCACCACTCTGGAGCATGGCTTCTCCCAGACTGTGGTCCGCCTGGCT
             1960      1970      1980      1990      2000      2010

     2290      2300      2310      2320      2330      2340
LEX151 CTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGCCAAAGCCAGAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGCCAAAGCCAGAG
             2020      2030      2040      2050      2060      2070

     2350      2360      2370      2380      2390      2400
LEX151 GAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCACCCAAGGCCTGGTACAAGGACATC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 GAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCACCCAAGGCCTGGTACAAGGACATC
             2080      2090      2100      2110      2120      2130

     2410      2420      2430      2440      2450      2460
```

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LEX151 CTGCAGCTCATTGGCTTCGCCAACCTGCCCCGGGTGGATGAGTACTGTGAGCGCGTGTGG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 CTGCAGCTCATTGGCTTCGCCAACCTGCCCCGGGTGGATGAGTACTGTGAGCGCGTGTGG
               2140      2150      2160      2170      2180      2190

    2470      2480      2490      2500      2510      2520
LEX151 TGCAGGGGCACCACGGAATGCTCAGGCTGCTTCCGGAGCCGGAGCCGGGGCAAGCAGGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 TGCAGGGGCACCACGGAATGCTCAGGCTGCTTCCGGAGCCGGAGCCGGGGCAAGCAGGCC
               2200      2210      2220      2230      2240      2250

    2530      2540      2550      2560      2570      2580
LEX151 AGGGGCAAGAGCTGGGCAGGGCTGGAGCTAGGCAAGAAGATGAAGAGCCGGGTGCATGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|897 AGGGGCAAGAGCTGGGCAGGGCTGGAGCTAGGCAAGAAGATGAAGAGCCGGGTGCATGCC
               2260      2270      2280      2290      2300      2310

    2590      2600      2610      2620
LEX151 GAGCACAATCGGACGCCCCGGGAGGTGGAGGCCACGTAG
       :::::::::::::::::::::::::::::::::::::::
gi|897 GAGCACAATCGGACGCCCCGGGAGGTGGAGGCCACGTAGAAGGGGGCAGAGGAGGGGTGG
               2320      2330      2340      2350      2360      2370

gi|897 TCAGGATGGGCTGGGGGGCCCACTAGCAGCCCCCAGCATCTCCCACCCACCCAGCTAGGG
               2380      2390      2400      2410      2420      2430

>>gi|8978201|dbj|AB029496.1| Homo sapiens mRNA for semap  (4700 nt)
rev-comp initn:  83 init1:  83 opt:  95
 67.105% identity in 76 nt overlap (119-46:407-475)

    150       140       130       120       110       100
LEX15- GCGGGAAGAGGGGCGGAGGAGAGAAGGAGGCTGGGGCCTTGCCGTCCACCTGCCGCTTCT
                                   :::::::::: : : :::::::   :  ::
gi|897 ACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGCC--CT
          380       390       400       410       420       430

     90        80        70        60        50        40
LEX15- CCTTCCACCTTGTTGGCC-CAGTGCAG-GCTTTTGTGCCACACTGGCCAGCTCCCCATTG
       : :  ::     ::::::: : :::  : :: : ::   :::: ::::
gi|897 CATCACA----GTTGGCCACCGTGGGGAGCATGTGCTCCAC-CTGGAGCCTGGCAGTGTG
            440       450       460       470       480

     30        20        10
LEX15- GGAAGACCTTCCCAGCTAGGGCACAGGCCAT

gi|897 GAAAGTGGCCGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATA
        490       500       510       520       530       540


2628 residues in 1 query   sequences
4700 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Fri Sep 19 13:50:44 2003 done: Fri Sep 19 13:50:45 2003
 Scan time:  0.117 Display time:  0.133

Function used was FASTA
```

Home **Paracel BLAST Results** Help

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.fa
26,679 sequences; 200,800,637,119 total letters

Query= 1
(2629 letters)

```
                                                                 Score     E
Sequences producing significant alignments:                      (bits)  Value

AC006208.3.1.123943                                               940    0.0
AC000063.1.1.34478                                                 72    2e-09
AC079799.7.1.172495                                                54    5e-04

>AC006208.3.1.123943
          Length = 123943

 Score =  940 bits (474), Expect = 0.0
 Identities = 474/474 (100%)
 Strand = Plus / Minus


Query: 2156  caggtgaagacggacgagcgagtcttgcacacggagcgggggctgctgttccgcaggctt 2215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44516 caggtgaagacggacgagcgagtcttgcacacggagcgggggctgctgttccgcaggctt 44457


Query: 2216  agccgtttcgatgcgggcacctacacctgcaccactctggagcatggcttctcccagact 2275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44456 agccgtttcgatgcgggcacctacacctgcaccactctggagcatggcttctcccagact 44397


Query: 2276  gtggtccgcctggctctggtggtgattgtggcctcacagctggacaacctgttccctccg 2335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44396 gtggtccgcctggctctggtggtgattgtggcctcacagctggacaacctgttccctccg 44337


Query: 2336  gagccaaagccagaggagcccccagcccggggaggcctggcttccaccccacccaaggcc 2395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44336 gagccaaagccagaggagcccccagcccggggaggcctggcttccaccccacccaaggcc 44277


Query: 2396  tggtacaaggacatcctgcagctcattggcttcgccaacctgccccgggtggatgagtac 2455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44276 tggtacaaggacatcctgcagctcattggcttcgccaacctgccccgggtggatgagtac 44217


Query: 2456  tgtgagcgcgtgtggtgcaggggcaccacggaatgctcaggctgcttccggagccggagc 2515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44216 tgtgagcgcgtgtggtgcaggggcaccacggaatgctcaggctgcttccggagccggagc 44157
```

```
Query: 2516  cggggcaagcaggccaggggcaagagctgggcagggctggagctaggcaagaagatgaag 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44156 cggggcaagcaggccaggggcaagagctgggcagggctggagctaggcaagaagatgaag 44097

Query: 2576  agccgggtgcatgccgagcacaatcggacgccccgggaggtggaggccacgtag 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 44096 agccgggtgcatgccgagcacaatcggacgccccgggaggtggaggccacgtag 44043
```

```
 Score =  781 bits (394), Expect = 0.0
 Identities = 394/394 (100%)
 Strand = Plus / Minus
```

```
Query: 2     atggcctgtgccctagctgggaaggtcttcccaatggggagctggccagtgtggcacaaa 61
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53746 atggcctgtgccctagctgggaaggtcttcccaatggggagctggccagtgtggcacaaa 53687

Query: 62    agcctgcactgggccaacaaggtggaaggagaagcggcaggtggacggcaaggccccagc 121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53686 agcctgcactgggccaacaaggtggaaggagaagcggcaggtggacggcaaggccccagc 53627

Query: 122   ctccttctctcctccgcccctcttcccgcccaggactgggtggagccactgccttataag 181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53626 ctccttctctcctccgcccctcttcccgcccaggactgggtggagccactgccttataag 53567

Query: 182   tggtggcctggtggcagcagagcaaactacaaccggcggccagcgggaccagagggcggc 241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53566 tggtggcctggtggcagcagagcaaactacaaccggcggccagcgggaccagagggcggc 53507

Query: 242   tctgcaggcaggcggcagcggtgccctcagttccccagcatggcccccctcggcctgggcc 301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53506 tctgcaggcaggcggcagcggtgccctcagttccccagcatggcccccctcggcctgggcc 53447

Query: 302   atttgctggctgctagggggcctcctgctccatgggggtagctctggccccagccccggc 361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53446 atttgctggctgctagggggcctcctgctccatgggggtagctctggccccagccccggc 53387

Query: 362   cccagtgtgccccgcctgcggctctcctaccgag 395
             ||||||||||||||||||||||||||||||||||
Sbjct: 53386 cccagtgtgccccgcctgcggctctcctaccgag 53353
```

```
 Score =  462 bits (233), Expect = e-127
 Identities = 233/233 (100%)
 Strand = Plus / Minus
```

```
Query: 1423  gtgccccagcaagatgaccgcacagccaggacggcctttggcagcaccaaggactaccc 1482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 48539 gtgccccagcaagatgaccgcacagccaggacggccttttggcagcaccaaggactaccc 48480

Query: 1483  agatgaggtgctgcagtttgcccgagcccacccccctcatgttctggcctgtgcggcctcg 1542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48479 agatgaggtgctgcagtttgcccgagcccacccccctcatgttctggcctgtgcggcctcg 48420

Query: 1543  acatggccgccctgtccttgtcaagacccacctggcccagcagctacaccagatcgtggt 1602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48419 acatggccgccctgtccttgtcaagacccacctggcccagcagctacaccagatcgtggt 48360

Query: 1603  ggaccgcgtggaggcagaggatgggacctacgatgtcattttcctggggactg 1655
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48359 ggaccgcgtggaggcagaggatgggacctacgatgtcattttcctggggactg 48307


 Score =  456 bits (230), Expect = e-125
 Identities = 230/230 (100%)
 Strand = Plus / Minus

Query: 1789  gcaaatgctatacgtgggctctcggctgggtgtggcccagctgcggctgcaccaatgtga 1848
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46640 gcaaatgctatacgtgggctctcggctgggtgtggcccagctgcggctgcaccaatgtga 46581

Query: 1849  gacttacggcactgcctgtgcagagtgctgcctggcccgggacccatactgtgcctggga 1908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46580 gacttacggcactgcctgtgcagagtgctgcctggcccgggacccatactgtgcctggga 46521

Query: 1909  tggtgcctcctgtacccactaccgccccagccttggcaagcgccggttccgccggcagga 1968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46520 tggtgcctcctgtacccactaccgccccagccttggcaagcgccggttccgccggcagga 46461

Query: 1969  catccggcacggcaaccctgccctgcagtgcctgggccagagccaggaag 2018
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46460 catccggcacggcaaccctgccctgcagtgcctgggccagagccaggaag 46411


 Score =  327 bits (165), Expect = 2e-86
 Identities = 165/165 (100%)
 Strand = Plus / Minus

Query: 394   agacctcctgtctgccaaccgctctgccatctttctgggcccccagggctccctgaacct 453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51349 agacctcctgtctgccaaccgctctgccatctttctgggcccccagggctccctgaacct 51290

Query: 454   ccaggccatgtacctagatgagtaccgagaccgcctctttctgggtggcctggacgccct 513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51289 ccaggccatgtacctagatgagtaccgagaccgcctctttctgggtggcctggacgccct 51230
```

```
Query: 514   ctactctctgcggctggaccaggcatggccagatccccgggaggt 558
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51229 ctactctctgcggctggaccaggcatggccagatccccgggaggt 51185


 Score =  294 bits (148), Expect = 3e-76
 Identities = 148/148 (100%)
 Strand = Plus / Minus


Query: 1276  cagtgccgtgttccagggcttcgccgtctgtgtgtaccacatggcagacatctgggaggt 1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48964 cagtgccgtgttccagggcttcgccgtctgtgtgtaccacatggcagacatctgggaggt 48905


Query: 1336  tttcaacgggccctttgcccaccgagatgggcctcagcaccagtgggggccctatggggg 1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48904 tttcaacgggccctttgcccaccgagatgggcctcagcaccagtgggggccctatggggg 48845


Query: 1396  caaggtgcccttccctcgccctggcgtg 1423
             ||||||||||||||||||||||||||||
Sbjct: 48844 caaggtgcccttccctcgccctggcgtg 48817


 Score =  292 bits (147), Expect = 1e-75
 Identities = 147/147 (100%)
 Strand = Plus / Minus


Query: 947   gacccccggtttgtgatggccgcccggatccctgagaactctgaccaggacaatgacaag 1006
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49850 gacccccggtttgtgatggccgcccggatccctgagaactctgaccaggacaatgacaag 49791


Query: 1007  gtgtacttcttcttctcggagacggtcccctcgcccgatggtggctcgaaccatgtcact 1066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49790 gtgtacttcttcttctcggagacggtcccctcgcccgatggtggctcgaaccatgtcact 49731


Query: 1067  gtcagccgcgtgggccgcgtctgcgtg 1093
             |||||||||||||||||||||||||||
Sbjct: 49730 gtcagccgcgtgggccgcgtctgcgtg 49704


 Score =  286 bits (144), Expect = 6e-74
 Identities = 145/146 (99%)
 Strand = Plus / Minus


Query: 2017  agaagaggcagtgggacttgtggcagccaccatggtctacggcacggagcacaatagcac 2076
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46108 agaagaggcagtgggacttgtggcagccaccatggtctacggcacggagcacaatagcac 46049


Query: 2077  cttcctggagtgcctgcccaagtctccccargctgctgtgcgctggctcttgcagaggcc 2136
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
```

```
Sbjct: 46048 cttcctggagtgcctgcccaagtctccccaggctgctgtgcgctggctcttgcagaggcc 45989

Query: 2137  aggggatgaggggcctgaccaggtga 2162
             ||||||||||||||||||||||||||
Sbjct: 45988 aggggatgaggggcctgaccaggtga 45963


 Score =  240 bits (121), Expect = 3e-60
 Identities = 121/121 (100%)
 Strand = Plus / Minus

Query: 619   gacagagtgcgccaacttcgtgcgggtgctacagcctcacaaccggacccacctgctagc 678
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50745 gacagagtgcgccaacttcgtgcgggtgctacagcctcacaaccggacccacctgctagc 50686

Query: 679   ctgtggcactggggccttccagcccacctgtgccctcatcacagttggccaccgtgggga 738
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50685 ctgtggcactggggccttccagcccacctgtgccctcatcacagttggccaccgtgggga 50626

Query: 739   g 739
             |
Sbjct: 50625 g 50625


 Score =  236 bits (119), Expect = 5e-59
 Identities = 119/119 (100%)
 Strand = Plus / Minus

Query: 829   agacggggagctgtacacgggtctcactgctgacttcctggggcgagaggccatgatctt 888
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50132 agacggggagctgtacacgggtctcactgctgacttcctggggcgagaggccatgatctt 50073

Query: 889   ccgaagtggaggtcctcggccagctctgcgttccgactctgaccagagtctcttgcacg 947
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50072 ccgaagtggaggtcctcggccagctctgcgttccgactctgaccagagtctcttgcacg 50014


 Score =  230 bits (116), Expect = 3e-57
 Identities = 116/116 (100%)
 Strand = Plus / Minus

Query: 1093  gaatgatgctgggggccagcgggtgctggtgaacaaatggagcactttcctcaaggccag 1152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49489 gaatgatgctgggggccagcgggtgctggtgaacaaatggagcactttcctcaaggccag 49430

Query: 1153  gctggtctgctcggtgcccggccctggtggtgccgagacccactttgaccagctag 1208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49429 gctggtctgctcggtgcccggccctggtggtgccgagacccactttgaccagctag 49374
```

```
 Score =  188 bits (95), Expect = 1e-44
 Identities = 95/95 (100%)
 Strand = Plus / Minus


Query: 1655  gactcagggtctgtgctcaaagtcatcgctctccaggcagggggctcagctgaacctgag 1714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48212 gactcagggtctgtgctcaaagtcatcgctctccaggcagggggctcagctgaacctgag 48153

Query: 1715  gaagtggttctggaggagctccaggtgtttaaggt 1749
             |||||||||||||||||||||||||||||||||||
Sbjct: 48152 gaagtggttctggaggagctccaggtgtttaaggt 48118


 Score =  184 bits (93), Expect = 2e-43
 Identities = 93/93 (100%)
 Strand = Plus / Minus


Query: 738   agcatgtgctccacctggagcctggcagtgtggaaagtggccgggggcggtgccctcacg 797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50351 agcatgtgctccacctggagcctggcagtgtggaaagtggccgggggcggtgccctcacg 50292

Query: 798   agcccagccgtccctttgccagcaccttcatag 830
             |||||||||||||||||||||||||||||||||
Sbjct: 50291 agcccagccgtccctttgccagcaccttcatag 50259


 Score =  143 bits (72), Expect = 6e-31
 Identities = 72/72 (100%)
 Strand = Plus / Minus


Query: 1207  agaggatgtgttcctgctgtggcccaaggccgggaagagcctcgaggtgtacgcgctgtt 1266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 49265 agaggatgtgttcctgctgtggcccaaggccgggaagagcctcgaggtgtacgcgctgtt 49206

Query: 1267  cagcaccgtcag 1278
             ||||||||||||
Sbjct: 49205 cagcaccgtcag 49194


 Score =  129 bits (65), Expect = 9e-27
 Identities = 65/65 (100%)
 Strand = Plus / Minus


Query: 555   aggtcctgtggccaccgcagccaggacagagggaggagtgtgttcgaaagggaagagatc 614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 51063 aggtcctgtggccaccgcagccaggacagagggaggagtgtgttcgaaagggaagagatc 51004
```

```
Query: 615    ctttg 619
              |||||
Sbjct: 51003  ctttg 50999
```

```
 Score = 87.8 bits (44), Expect = 3e-14
 Identities = 44/44 (100%)
 Strand = Plus / Minus
```

```
Query: 1746   aggtgccaacacctatcaccgaaatggagatctctgtcaaaagg 1789
              ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 47403  aggtgccaacacctatcaccgaaatggagatctctgtcaaaagg 47360
```

```
>AC000063.1.1.34478
          Length = 34478

 Score = 71.9 bits (36), Expect = 2e-09
 Identities = 48/52 (92%)
 Strand = Plus / Minus
```

```
Query: 1860 ctgcctgtgcagagtgctgcctggcccgggacccatactgtgcctgggatgg 1911
            |||||||||| || |||||||| ||||||||||| |||||||||||||||||
Sbjct: 5711 ctgcctgtgctgactgctgccttgcccgggacccttactgtgcctgggatgg 5660
```

```
>AC079799.7.1.172495
          Length = 172495

 Score = 54.0 bits (27), Expect = 5e-04
 Identities = 42/47 (89%)
 Strand = Plus / Minus
```

```
Query: 1865   tgtgcagagtgctgcctggcccgggacccatactgtgcctgggatgg 1911
              ||||| || ||||||||||| || ||||| |||||||||||||||||
Sbjct: 151014 tgtgctgactgctgcctggctcgagacccttactgtgcctgggatgg 150968
```

```
  Database: Homo_sapiens.latestgp.fa
    Posted date:  Jul 8, 2003 12:51 PM
  Number of letters in database: 200,800,637,119
  Number of sequences in database:  26,679

Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
```

```
Number of Hits to DB: 0
length of query: 5260
length of database: 200,800,637,119
effective HSP length: 22
effective length of query: 2607
effective search space used:        0
T: 0
A: 0
X1: 0 ( 0.0 bits)
X2: 20 (39.7 bits)
S1: 12 (24.3 bits)
S2: 24 (48.1 bits)
```